

Run on: March 26, 2005, 14:36:30 ; Search time 22 Seconds  
 (without alignments)  
 78.042 Million cell

updates/sec

Title: US-10-009-643-5  
 Perfect score: 111  
 Sequence: 1 SKAYRKLLGQLSARLYLHSLMAK 23

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 500 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
 score greater than or equal to the score of the result being  
 printed,  
 and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	104	93.7	29	3	US-08-789-329C-20	Sequence 20,
Appl						
2	104	93.7	43	3	US-08-789-329C-8	Sequence 8,
Appli						
3	104	93.7	46	3	US-08-789-329C-4	Sequence 4,
Appli						
4	104	93.7	172	3	US-08-789-329C-7	Sequence 7,
Appli						
5	104	93.7	175	3	US-08-789-329C-3	Sequence 3,
Appli						
6	97	87.4	45	1	US-08-062-472B-8	Sequence 8,
Appli						
7	97	87.4	173	1	US-08-062-472B-6	Sequence 6,
Appli						
8	96	86.5	45	1	US-08-062-472B-25	Sequence 25,
Appl						
9	96	86.5	113	1	US-08-062-472B-11	Sequence 11,

Run on: March 26, 2005, 14:37:35 ; Search time 48 Seconds  
(without alignments)  
158.653 Million cell

updates/sec

Title: US-10-009-643-5  
Perfect score: 111  
Sequence: 1 SKAYRKLLGQLSARLYLHSIMAK 23

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Published Applications\_AA:\*  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*  
3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*  
5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*  
6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*  
7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*  
8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*  
9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*  
10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*  
11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*  
12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*  
13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*  
14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*  
15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*  
16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*  
17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*  
18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*  
19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being  
printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query	Match	Length	ID	Description
No.				DB		
-----						
1	67	60.4	170	17	US-10-686-282-15	Sequence
15, Appl						
2	67	60.4	170	17	US-10-686-282-17	Sequence

Run on: March 26, 2005, 14:36:00 ; Search time 16 Seconds  
 (without alignments)  
 138.312 Million cell

updates/sec

Title: US-10-009-643-5  
 Perfect score: 111  
 Sequence: 1 SKAYRKLLGQLSARLYLHSLMAK 23

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 500 summaries

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
-----						
1	97	87.4	173	2	S34767	neuropeptides
prec						
2	80	72.1	176	2	A34044	pituitary
adenylat						
3	71	64.0	175	2	A37786	pituitary
adenylat						
4	67	60.4	145	2	A60038	vasoactive
intesti						
5	67	60.4	170	1	VRHU	vasoactive
intesti						
6	63	56.8	44	1	RHPG	somatoliberin
- pi						
7	63	56.8	108	1	RHHUS	somatoliberin
prec						
8	62	55.9	55	1	VRGP	vasoactive
intesti						
9	62	55.9	170	1	VRRT	vasoactive
intesti						
10	62	55.9	170	2	A60037	vasoactive
intesti						
11	62	55.9	195	2	I50456	pituitary
adenylat						
12	61	55.0	176	2	I84638	pituitary
adenylat						
13	60	54.1	44	1	RHBOS	somatoliberin

Run on: March 26, 2005, 14:35:35 ; Search time 55 Seconds  
 (without alignments)  
 214.142 Million cell

updates/sec

Title: US-10-009-643-5  
 Perfect score: 111  
 Sequence: 1 SKAYRKLLGQLSARLYLHSLMAK 23

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 500 summaries

Database : UniProt\_03:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

# SUMMARIES

Result		%					
No.	Score	Query Match	Length	DB	ID	Description	
-----							
1	104	93.7	175	1	PACA_CHICK	P41534	g
glucagon-							
2	97	87.4	173	1	PACA_ONCNE	P41585	
oncorhynchu							
3	97	87.4	173	2	Q98SP5	Q98sp5	
oncorhynchu							
4	94	84.7	45	1	SLIB_CYPCA	P42692	
cyprinus ca							
5	94	84.7	89	2	Q98SP6	Q98sp6	anas
platyr							
6	94	84.7	171	1	PACA_RANRI	Q09169	r
glucagon-							
7	94	84.7	172	2	Q9DE29	Q9de29	
brachydanio							
8	81	73.0	176	1	PACA_PIG	P41535	s
pituitary							
9	80	72.1	176	1	PACA_SHEEP	P16613	o
pituitary							
10	78	70.3	171	2	Q9PUF8	Q9puf8	
xenopus lae							
11	71	64.0	175	1	PACA_RAT	P13589	r
pituitary							

Run on: March 26, 2005, 01:33:19 ; Search time 314 Seconds  
 (without alignments)  
 8801.501 Million cell

updates/sec

Title: US-10-009-643-3  
 Perfect score: 1689  
 Sequence: 1 taaggaagataaaagaatta.....atactcagtccttcacacaga  
 1689

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
 6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
-----					
1	484.6	28.7	1272	1	US-08-073-799C-7
Appli					Sequence 7,
2	484.6	28.7	1272	1	US-07-947-672-7
Appli					Sequence 7,
3	484.6	28.7	1272	1	US-08-432-043-7
Appli					Sequence 7,
4	484.6	28.7	1272	2	US-08-660-963-7
Appli					Sequence 7,
5	481.8	28.5	1617	4	US-09-016-434-1211
1211, Ap					Sequence
6	474.8	28.1	1257	1	US-07-946-232-7
Appli					Sequence 7,
7	469.6	27.8	1545	2	US-08-660-963-9
Appli					Sequence 9,
8	446.2	26.4	1983	1	US-08-073-799C-9
Appli					Sequence 9,
9	296.4	17.5	1455	2	US-08-811-897A-31
Appl					Sequence 31,
10	296.4	17.5	1455	2	US-08-855-213-31
					Sequence 31,

Run on: March 26, 2005, 01:53:48 ; Search time 926 Seconds  
 (without alignments)  
 10869.667 Million cell

updates/sec

Title: US-10-009-643-3  
 Perfect score: 1689  
 Sequence: 1 taaggaagataaaagaatta.....atactcagtccttcacacaga  
 1689

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 5552208 seqs, 2979665951 residues

Total number of hits satisfying chosen parameters: 11104416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications\_NA:\*  
 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*  
 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*  
 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*  
 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*  
 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq:\*  
 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*  
 7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq:\*  
 8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*  
 9: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*  
 10: /cgn2\_6/ptodata/1/pubpna/US09E\_PUBCOMB.seq:\*  
 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*  
 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq:\*  
 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq:\*  
 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq:\*  
 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*  
 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq:\*  
 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*  
 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq:\*  
 19: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq:\*  
 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*  
 21: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq:\*  
 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

#### SUMMARIES

Result	Score	Match	Length	DB	ID	Description
1	481.8	28.5	1617	14	US-10-147-087-3	Sequence 3,
2	481.8	28.5	1617	15	US-10-171-581-230	Sequence
3	481.8	28.5	1617	15	US-10-225-567A-141	Sequence

Run on: March 26, 2005, 01:26:25 ; Search time 5069 Seconds  
 (without alignments)  
 12683.084 Million cell

updates/sec

Title: US-10-009-643-3  
 Perfect score: 1689  
 Sequence: 1 taaggaagataaaagaatta.....atactcagtccttcacacaga  
 1689

Scoring table: IDENTITY\_NUC  
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : EST:\*  
 1: gb\_est1:\*  
 2: gb\_est2:\*  
 3: gb\_htc:\*  
 4: gb\_est3:\*  
 5: gb\_est4:\*  
 6: gb\_est5:\*  
 7: gb\_est6:\*  
 8: gb\_gss1:\*  
 9: gb\_gss2:\*

# SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	485	28.7	621	4	BM490642	BM490642
pgp2n.pk0						
2	437.4	25.9	1551	3	AK030504	AK030504 Mus
muscu						
3	412.2	24.4	1272	9	AY416892	AY416892 Homo
sapi						
4	394.6	23.4	1272	9	AY416894	AY416894 Mus
muscu						
5	355	21.0	1146	9	AY416893	AY416893 Pan
trogl						
6	292.6	17.3	1407	9	AY400569	AY400569 Homo
sapi						
7	291.4	17.3	1407	9	AY400570	AY400570 Pan
trogl						
8	291	17.2	2583	3	AK052465	AK052465 Mus
muscu						
9	286.8	17.0	1407	9	AY400571	AY400571 Mus
muscu						

Run on: March 26, 2005, 14:27:54 ; Search time 71 Seconds  
 (without alignments)  
 2282.431 Million cell

updates/sec

Title: US-10-009-643-4  
 Perfect score: 2272  
 Sequence: 1 MSYHCVLYTLTLAVLVAGNV.....RRTRWTVPTSSGVKMNTSVC 419

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
 1: geneseqp1980s:\*  
 2: geneseqp1990s:\*  
 3: geneseqp2000s:\*  
 4: geneseqp2001s:\*  
 5: geneseqp2002s:\*  
 6: geneseqp2003as:\*  
 7: geneseqp2003bs:\*  
 8: geneseqp2004s:\*

# SUMMARIES

Result		%	Query					
No.	Score	Match	Length	DB	ID			Description
1	2272	100.0	419	4	AAB19981			Aab19981
Chicken g								
2	1419.5	62.5	423	2	AAR51072			Aar51072
Human Gro								
3	1419.5	62.5	423	2	AAW10488			Aaw10488
Human acr								
4	1419.5	62.5	423	2	AAW24033			Aaw24033
Growth ho								
5	1419.5	62.5	423	2	AAW67744			Aaw67744
Human clo								
6	1419.5	62.5	423	4	AAB71873			Aab71873
Human GRF								
7	1419.5	62.5	423	7	ADC86187			Adc86187
Human GPC								
8	1419.5	62.5	423	8	ADH34649			Adh34649
Growth ho								
9	1419.5	62.5	423	8	ADO29355			Ado29355



Run on: March 26, 2005, 14:31:19 ; Search time 21 Seconds  
 (without alignments)  
 1489.427 Million cell

updates/sec

Title: US-10-009-643-4  
 Perfect score: 2272  
 Sequence: 1 MSYHCVLYTLTLAVLVAGNV.....RRTRWTVPTSSGVKMNTSVC 419

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
 1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*  
 2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*  
 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*  
 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*  
 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*  
 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

# SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1419.5	62.5	423	1	US-08-073-799C-8	Sequence 8,
Appli						
2	1419.5	62.5	423	1	US-07-947-672-8	Sequence 8,
Appli						
3	1419.5	62.5	423	1	US-08-432-043-8	Sequence 8,
Appli						
4	1419.5	62.5	423	2	US-08-660-963-8	Sequence 8,
Appli						
5	1419.5	62.5	423	4	US-09-631-603-18	Sequence 18,
Appl						
6	1397.5	61.5	418	1	US-07-946-232-8	Sequence 8,
Appli						
7	1313.5	57.8	513	2	US-08-660-963-11	Sequence 11,
Appl						
8	1313	57.8	457	2	US-08-660-963-10	Sequence 10,
Appl						
9	1035	45.6	459	4	US-09-694-519-4	Sequence 4,
Appli						
10	1012	44.5	459	4	US-09-694-519-3	Sequence 3,
Appli						
11	1012	44.5	459	4	US-09-694-519-8	Sequence 8,
Appli						

Run on: March 26, 2005, 14:32:59 ; Search time 50 Seconds  
 (without alignments)  
 2774.626 Million cell

updates/sec

Title: US-10-009-643-4  
 Perfect score: 2272  
 Sequence: 1 MSYHCVLYTLTLAVLVAGNV.....RRTRWTVPTSSGVKMNTSVC 419

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep:\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep:\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
-----						
1	1419.5	62.5	423	15	US-10-292-798-640	Sequence
640, App						
2	1414.5	62.3	423	14	US-10-147-087-4	Sequence 4,
Appli						
3	1414.5	62.3	423	14	US-10-225-567A-142	Sequence
142, App						
4	1243	54.7	476	14	US-10-017-161-730	Sequence
730, App						

Run on: March 26, 2005, 14:30:29 ; Search time 16 Seconds  
 (without alignments)  
 2519.676 Million cell

updates/sec

Title: US-10-009-643-4  
 Perfect score: 2272  
 Sequence: 1 MSYHCVLYTLTLAVLVAGNV.....RRTRWTVPTSSGVKMNTSVC 419

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR\_79:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

# SUMMARIES

Result No.	Score	Query Match Length DB ID	Description
-----			
----			
1	1414.5	62.3 423 2 A45363	somatoliberin
rece			
2	1352.5	59.5 451 2 I46586	growth
hormone-rel			
3	1274.5	56.1 464 2 S29754	growth
hormone-rel			
4	1274	56.1 423 2 S29753	growth
hormone-rel			
5	1012	44.5 459 2 JH0594	vasoactive
intesti			
6	985.5	43.4 467 2 JN0616	pituitary
adenylat			
7	977.5	43.0 525 2 JN0902	pituitary
adenylat			
8	973	42.8 495 2 JC2195	vasoactive
intesti			
9	971.5	42.8 460 2 JC2194	vasoactive
intesti			
10	961.5	42.3 495 2 S39061	pituitary

Run on: March 26, 2005, 14:29:49 ; Search time 58 Seconds  
 (without alignments)  
 3699.331 Million cell

updates/sec

Title: US-10-009-643-4  
 Perfect score: 2272  
 Sequence: 1 MSYHCVLYTLTLAVLVAGNV.....RRTRWTVPTSSGVKMNTSVC 419

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : UniProt\_03:\*  
 1: uniprot\_sprot:\*  
 2: uniprot\_trembl:\*

# SUMMARIES

		%		Query			ID	Description
Result	Score	Match	Length	DB				
No.								
-----								
----								
1	1419.5	62.5	423	1	GRFR_HUMAN		Q02643	homo
sapien								
2	1366.5	60.1	423	1	GRFR_PIG		P34999	sus
scrofa								
3	1365	60.1	423	2	Q9BDH9		Q9bdh9	bos
taurus								
4	1360	59.9	423	2	Q9N1F8		Q9n1f8	bos
taurus								
5	1339	58.9	441	2	Q9TUJ0		Q9tuj0	bos
taurus								
6	1313	57.8	407	2	Q9BDI0		Q9bdi0	ovis
aries								
7	1297	57.1	439	2	Q9WU99		Q9wu99	rattus
norv								
8	1279.5	56.3	464	1	GRFR_RAT		Q02644	rattus
norv								
9	1274.5	56.1	464	2	Q6LEF5		Q6lef5	rattus
sp.								
10	1274	56.1	423	1	GRFR_MOUSE		P32082	mus